

GGAGGGCAGCAAGGACGGCACCAAGGGAGCTACCCCATGGACAGGGCCCCACAGAGACACCACCGGACAT
 CTCGGGAGCTGCTGGCTGCAAAGAAGACCCACACCTCACAAATTGAAGTGATCCCTTGCAAGATCTGTGG
 GGACAAGTCATCTGGGATCCACTACGGGGTTATCACCTGTGAGGGGTGCAAGGGCTTCTTCCGCCGCAGC
 CAGCAGTGTAATGTGGCCTACTCCTGCACGCGTCAGCAGAACTGCCCCATTGACCGAACCAGCCGCAACC
 GATGCCAGCATTGCCGCTGCAGAAGTGCTGGCTCTGGGCATGTCCCGAGATGCTGTCAAGTTTGGCCG
 AATGTCCAAGAAGCAGAGGGGACAGTCTACATGCAGAAGTGCAAGAACTGCAACAGCAGCAGCAACAG
 GAACAAGTGCCCAAGACTCCTCCAGCTGGGAGCCGCGGAGCAGACACACTTACATACACTTTAGGGCTCT
 CAGATGGGCAGCTACCACTGGGCGCCTCACCTGACCTACCCGAGGCCCTCTGCTTGTCCCCCTGGCCTCCT
 GAGAGCCTCAGGCTCTGGCCCCACCATATTCCAATACCTTGGCCAAAACAGAGGTCCAGGGGGCCTCCTGC
 CACCTTGAGTATAGTCCAGAACGAGGCAAAGCTGAAGGCAGAGACAGCATCTATAGCACTGACGGCCAAAC
 TTACTCTTGGAAGATGTGGACTTCGTTTTTGAGGAAACCAGGCATCCTGAACTTGGGGAACCAGAACAGGG
 TCCAGACAGCCACTGCATTCCAGTTTCTGCAGTGCCCCAGAGGTACCATATGCCTCTCTGACAGACATA
 GAGTACCTGGTACAGAATGTCTGCAAGTCCTTCCGAGAGACATGCCAGCTGCGACTGGAGGACCTTCTAC
 GGCAGCGCACCAACCTCTTTTACGGGAGGAGGTGACCAGCTACCAGAGGAAGTCAATGTGGGAGATGTG
 GGAGCGCTGTGCCACCACCTCACTGAGGCCATTCACTATGTGGTGGAGTTTGCCAAGCGGCTTTTCAGGC
 TTCATGGAGCTCTGCCAGAATGACCAGATCATACTACTGACAGCAGGAGCAATGGAAGTCGTCTTAGTCA
 GAATGTGCAGGGCCTACAATGCCAACACACAGTCTTTTTTGAAGGCAAATACGGTGGTGTGGAGCT
 GTTTCGAGCCTTGGGCTGCAGCGAGCTCATCAGCTCCATATTTGACTTTTCCCACTTCTCAGCGCCCTG
 TGTTTTTCTGAGGATGAGATTGCCCTCTACACGGCCCTGGTTCTCATCAATGCCAACCGTCTGGGCTCC
 AAGAGAAGAGGAGAGTGGAAACATCTGCAATACAATTTGGAAGTGGCTTTCCATCATCATCTCTGCAAGAC
 TCATCGACAAGGCCTCCTAGCCAAGCTGCCACCCAAAGGAAAACCTCCGGAGCCTGTGCAGCCAACATGTG
 GAAAAGCTGCAGATCTTCCAGCACCTCCACCCCATCGTGGTCCAAGCCGCCTTCCCNCCACTCTATAAGG
 AACTCTTCAGCACTGATGTTGAATCCCCTGAGGGGCTGTCAAAGTGATCTGGAGGAAGGACAACTTCTA
 TTTCCCTTCAGCCCTCTGACCCGTCTCCCTGGACTCCCTTACCCAGCCTTTCCCTTTCTGCACTCTATGA
 AGGGTGATATCCCTAGGAGTAAGCAAATCCTAAGACTGATTTTCTGCCCCCTAGGCTTGCCCTGTAGGACA
 ACAGCAGCAAGTGATGGAGAAAAGGCTTGTTATGTTTGTATTTCCATAAGTTCCACCCTGGCTTCTGGAA
 GCTGTGGGGTAGATGGGATAGAGATAGGATGACCAAGTCAAATAAAAAACAGACTGACAATCAGCAGGGA
 TAAATCCAGGTACCTGGGATAAGGAGAACTCAAATCTAGGCTTGAAAGCTAATAACAGTCCTTTCAATAC
 CTCATTGTATTTCCCATGGGTCTCCTGGGGGGACATGGATCTAGCTCAGAGACTGGTGGAAGCCCCC
 AGAAGGACCTGTATATAATAAGAATATAGATTCTGT (SEQ ID NO:1)

MDRAPQRHHRTSRELLAAKKTHTSQIEVIPCKICGDKSSGIHYGVITCEGCKGFFRRSQQCNVAYS
 CTRQQNCPIDRTSRNRCQHCRLQKCLALGMSRDAVKFGRMSKKQRDSLHAEVQKQLQQQQQQQE
 QVAKTPPAGSRGADTLTYTLGLSDGQLPLGASPDLPASACPPGLLRASGSGPPYSNTLAKTEVQG
 ASCHLEYSPERGKAEGRDSIYSTDGQLTLGRCGLRFEETRHPELGEPEQGPDSHCIPSFCSAPEVPY
 ASLTDIEYLQNVCKSFRETCLRLLEDLLRQRTNLFSSREEVTSYQRKSMWEMWERCAHHLTEAIQ
 YVVEFAKRLSGFMELCQNDQILLTAGAMEVVLVRMCRAYNANNHTVFFEGKYGGVELFRALGC
 SELISSIFDFSHFLSALCFSEDEIALYALVLINANRPLQEKRRVEHLQYNLELAFHHHLCKTHRQG
 LLAKLPPKGLRLSLCSQHVEKLQIFQHLHPIVVQAAPPLYKELFSTDVESPEGLSK (SEQ ID NO:2)

FIG. 1

underlined = deleted in targeting construct

green = sequence flanking Neo insert in targeting construct

GGAGGGCAGCAAGGACGGCACCAAGGGAGCTACCCCATGGACAGGGCCCCACAGAGACAC
CACCGGACATCTCGGGAGCTGCTGGCTGCAAAGAAGACCCACACCTCACAAATTGAAGTG
ATCCCTTGCAAGATCTGTGGGGACAAGTCATCTGGGATCCACTACGGGGTTATCACCTGT
GAGGGGTGCAAG [GGCTTCTTCCGCCGAGCCAGCAGTGTAAATGTGGCCTACTCCTGCACG
CGTCAGCAGAA] CTGCCCCATTGACCGAACCAGCCGCAACCGATGCCAGCATTGCCGCCTG
CAGAAGTGCTGGCTCTGGGCATGTCCCGAGATGCTGTCAAGTTTGGCCGAATGTCCAAG
AAGCAGAGGGACAGTCTACATGCAGAAGTGCAGAAACAACTGCAACAGCAGCAGCAACAG
GAACAAGTGCCCAAGACTCCTCCAGCTGGGAGCCGCGGAGCAGACACACTTA [CATACACT
TTAGGGCTCTCAGATGGGCAGCTACCACTGGGCGCCTCACCTGACCTACCCGAGGCCTCT
GCTTGTCCCCCTGGCCTCCTGAGAGCCTCAGGCTCTGGCCCACCATATTCCAATACCTTG
GCCAAAACAGAGGTCCAGGGGGCCTCCTGCCACCTTGAGTATAGTCCAGAACGAGGCAAA
GCTGAAGGCAGAGACAGCATCTATAGCACTGACGGCCAACCTTACTCTTGGAAGATGTGGA
CTTCGTTTTTGAGGAAACCAGGCATCCTGAACCTTGGGGAACCAGAACAGGGTCCAGACAGC
CACTGCATTCCCAGTTTTCTGCAGTGCCCCAGAGGTACCATATGCCTCTCTGACAGACATA
G] AGTACCTGGTACAGAATGTCTGCAAGTCCTTCCGAGAGACATGCCAGCTGCGACTGGAG
GACCTTCTACGGCAGCGCACCAACCTCTTTTTCACGGGAGGAGGTGACCAGCTACCAGAGG
AAGTCAATGTGGGAGATGTGGGAGCGCTGTGCCACCACCTCACTGAGGCCATTTCAGTAT
GTGGTGGAGTTTGCCAAGCGGCTTTCAGGCTTCATGGAGCTCTGCCAGAATGACCAGATC
ATACTACTGACAGCAGGAGCAATGGAAGTCGTCCTAGTCAGAATGTGCAGGGCCTACAAT
GCCAACAACCACACAGTCTTTTTTTGAAGGCAAATACGGTGGTGTGGAGCTGTTTCGAGCC
TTGGGCTGCAGCGAGCTCATCAGCTCCATATTTGACTTTTCCCACCTTCCTCAGCGCCCTG
TGTTTTTCTGAGGATGAGATTGCCCTCTACACGGCCCTGGTTCTCATCAATGCCAACCGT
CCTGGGCTCCAAGAGAAGAGGAGAGTGGAACATCTGCAATACAATTTGGAAGTGGCTTTC
CATCATCATCTCTGCAAGACTCATCGACAAGGCCTCCTAGCCAAGCTGCCACCCAAAGGA
AAACTCCGGAGCCTGTGCAGCCAACATGTGGAAGCTGCAGATCTTCAGCACCTCCAC
CCCATCGTGGTCCAAGCCGCCTTCCCNCCACTCTATAAGGAACTCTTCAGCACTGATGTT
GAATCCCCTGAGGGGCTGTCAAAGTGATCTGGAGGAAGGACAACCTTCTATTTCTTCAG
CCCTCTGACCCGTCTCCCTGGACTCCCTTCACCCAGCCTTTCCTTTCTGCACTCTATGA
AGGGTGGTATCCCTAGGAGTAAGCAAATCCTAAGACTGATTTTCTGCCCCCTAGGCTTGCC
TTGTAGGACAACAGCAGCAAGTGATGGAGAAAAGGCTTGTTATGTTTGATTTCCCATAG
TTCCACCCTGGCTTCTGGAAGCTGTGGGTTAGATGGGATAGAGATAGGATGACCAAGTCA
AATAAAAAACAGACTGACAATCAGCAGGGATAAATCCAGGTACCTGGGATAAGGAGAACT
CAAATCTAGGCTTGAAAGCTAATAACAGTCCTTTCAATACCTCATTGTATTTCCCATGG
GTCCCTCCTGGGGGGACATGGATCTAGCTCAGAGACTGGTGGAAGCCCCCAGAAGGACCT
GTATATAATAAGAATATAGATTCCCTG (SEQ ID NO:1)

FIG. 2A

Gene Sequence
Structure *

252 bp Sequence Deleted 472 bp

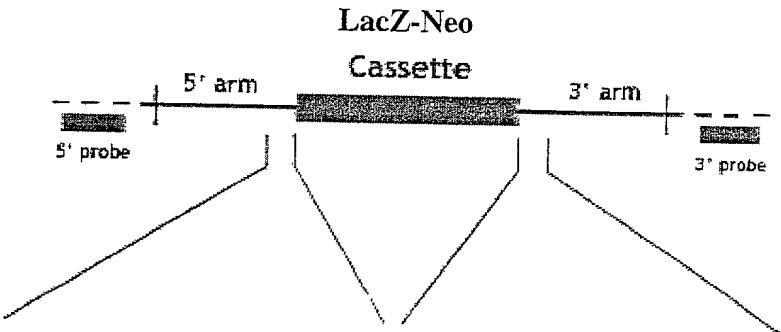
Size of full-length
cDNA: 2066 bp



Targeting Vector* (genomic sequence)

Construct Number: 651

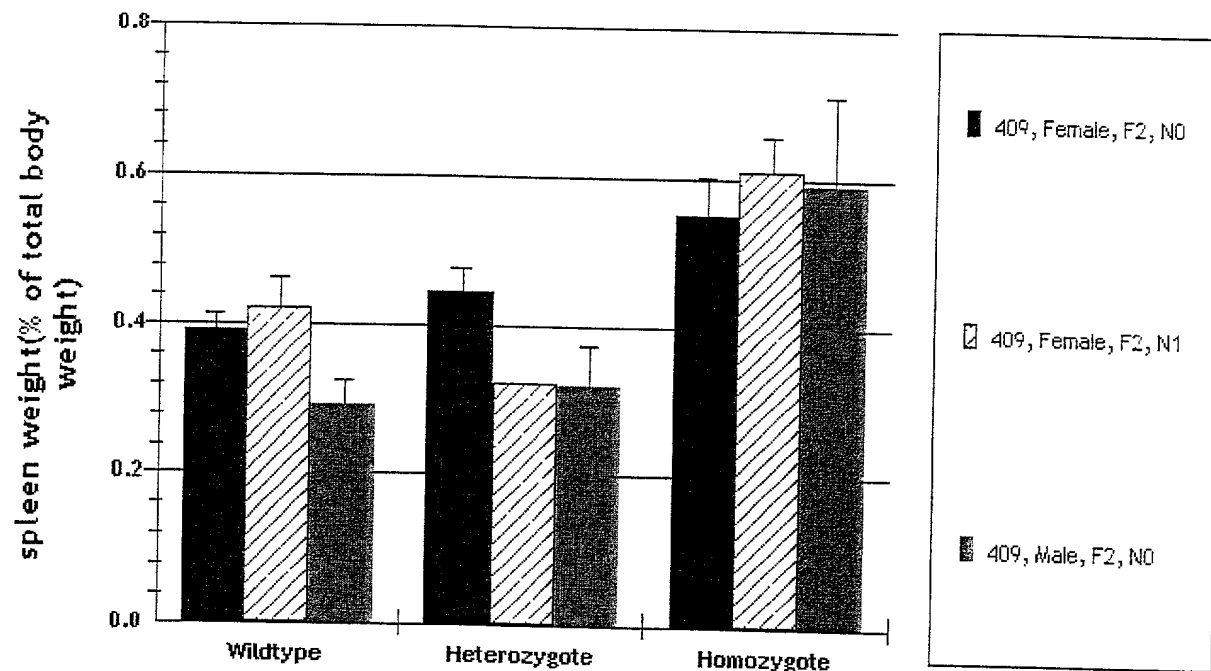
Arm Length:
5': 1.6 kb
3': 2.5 kb



<p>5'>CAGGGTCCATCACAATTATAC AGTGGAGGTTCTGGGACTTTGGTG GATGTAGAAATTCTTGAGACCAGT GCACATGAATTGGAGGTCCCTGGG ACCACCTCAAACCTCCGAGAGGGTG GGATAAGCAGTTTCTGTTTCCCAG GGCTTCTTCCGCCGAGCCAGCAG TGTAATGTGGCCTACTCCTGCACG CGTCAGCAGAA<3' (SEQ ID NO:3)</p>	<p>5'>CATACTTTAGGGCTCTCAG ATGGGCAGCTACCACTGGGCGCCT CACCTGACCTACCCGAGGCCTCTG CTTGTCCCCCTGGCCTCCTGAGAG CCTCAGGCTCTGGCCCACCATATT CCAATACCTTGGCCAAACAGAGG TCCAGGGGGCCTCCTGCCACCTTG AGTATAGTCCAGAACGAGGCAAAG CTGAAGGCAGA<3' (SEQ ID NO:4)</p>
---	--

FIG. 2B

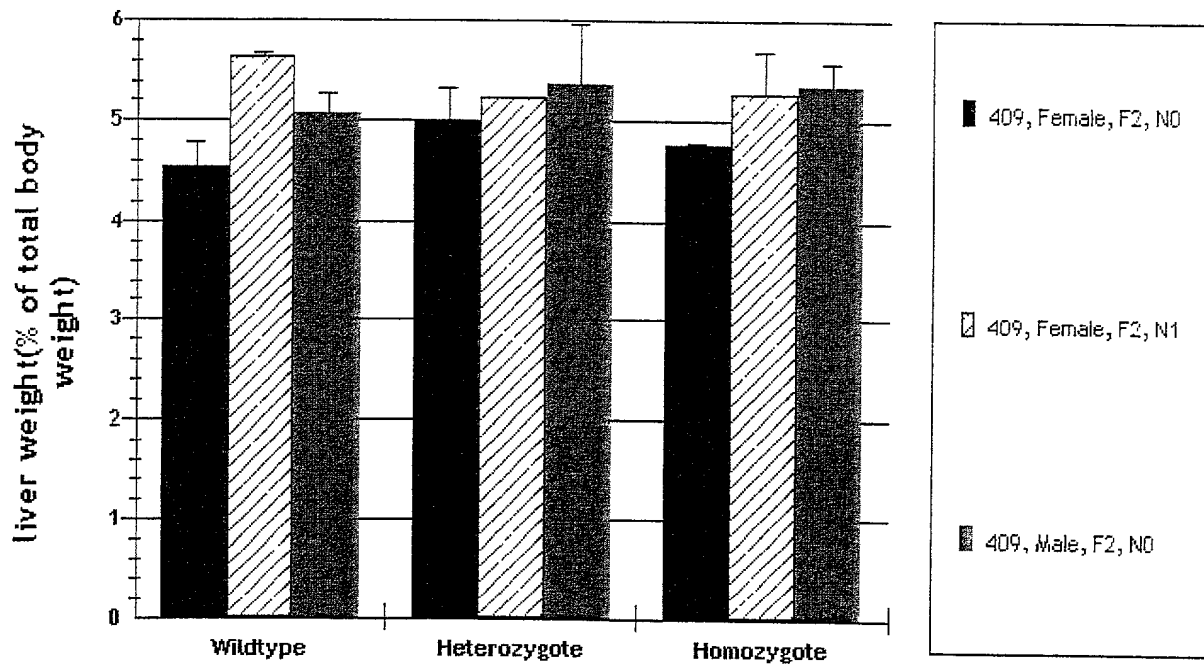
necropsy - spleen weight/body weight



© Deltagen, Inc.

FIG. 3

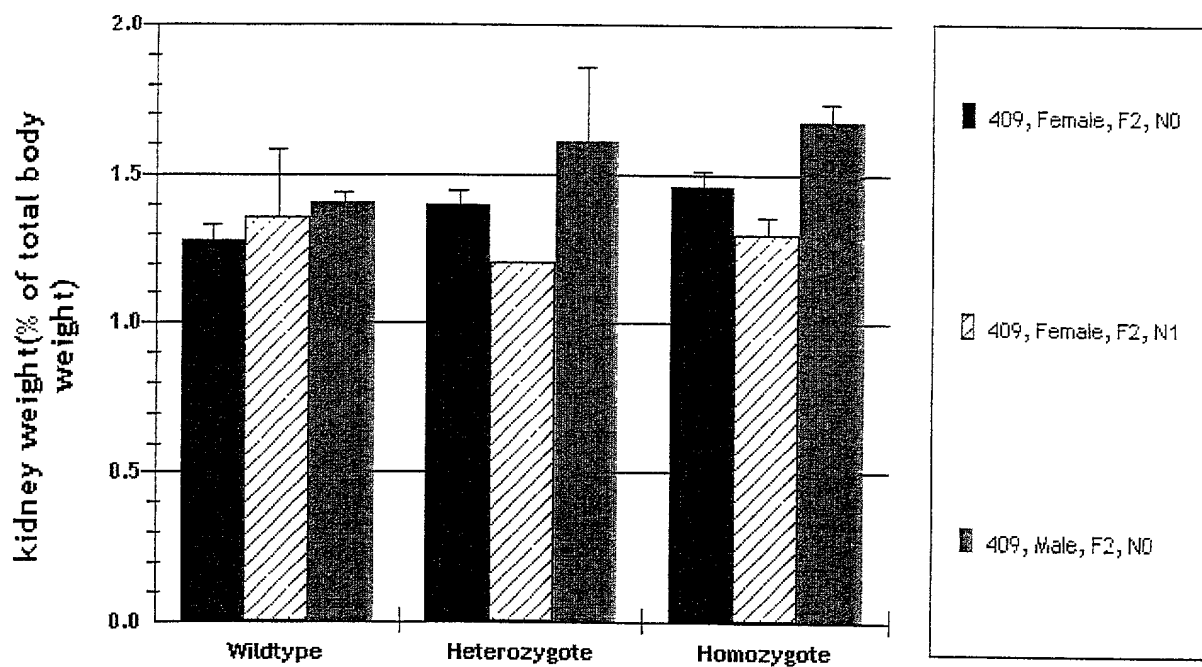
necropsy - liver weight/body weight



© Deltagen, Inc.

FIG. 4

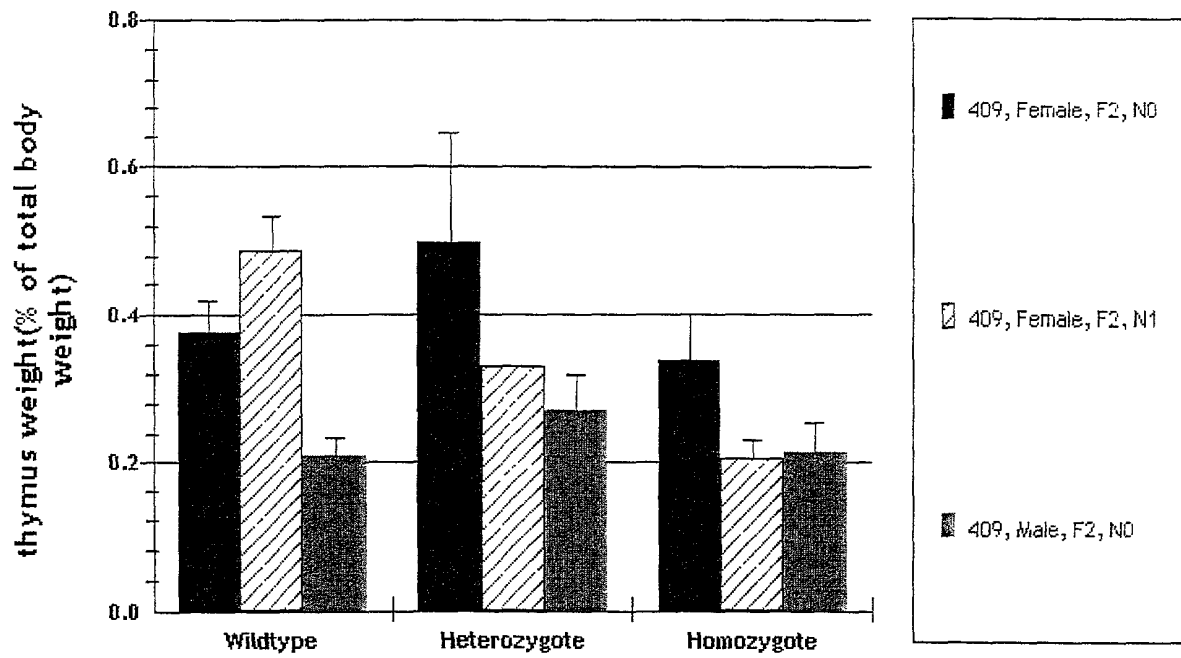
necropsy - kidney weight/body weight



© Deltagen, Inc.

FIG. 5

necropsy - thymus weight/body weight



© Deltagen, Inc.

FIG. 6